

GenCore version 5.1.4_p5_4578
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OM nucleic - protein search, using frame_plus_n2p model

Run on: April 1, 2003, 08:51:06 ; Search time 23.5 Seconds
(without alignments)
3478.165 Million cell updates/sec

Title: US-09-768-781-2
Perfect score: 2543
Sequence: 1 atgaacacagaccacacaa.....caaggcaagtgtgtctga 1389

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 262574 seqs, 29422922 residues
Total number of hits satisfying chosen parameters: 525148

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DB=Issued Patents AA -QPMT=faetan -SUFFIX=n2p.ra1 -MINMATCH=0.1 -LOOPEL=0
-LOOPEXT=0 -UNITS=Bits -START=1 -END=1 -MATRIX=blosom62 -TRANS-human40.cdi
-LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents AA:*
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5: /cgn2_6/ptodata/1/iaa/PCTUS.COMB.pcp.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	169	6.6	129	3	US-09-058-489-46
2	114	4.5	800	4	US-09-134-001C-5655
3	103.5	4.1	290	4	US-09-134-001C-4893
4	98.5	3.9	451	4	US-09-134-001C-4420
5	96.5	3.8	357	1	US-08-612-886-5
6	96.5	3.8	357	1	US-08-361-806A-5
7	96.5	3.8	357	5	PCT-US95-16806A-5
8	96.5	3.8	683	4	US-09-134-001C-5576
9	96	3.8	371	1	US-08-415-818-6
10	96	3.8	371	2	US-08-894-236-6
11	96	3.8	371	2	US-08-919-624-4
12	96	3.8	371	5	PCT-US96-01444-6

13	96	3.8	498	2	US-08-660-963-12	Sequence 12, Appl
14	95.5	3.8	255	2	US-09-154-802-3	Sequence 3, Appl
15	95.5	3.8	255	3	US-09-373-029-3	Sequence 3, Appl
16	95.5	3.8	325	3	US-08-706-281A-18	Sequence 18, Appl
17	95.5	3.8	325	4	US-09-097-231-18	Sequence 18, Appl
18	95	3.7	458	4	US-08-487-596-16	Sequence 16, Appl
19	92.5	3.6	325	1	US-08-671-525B-10	Sequence 10, Appl
20	92.5	3.6	325	1	US-08-672-109B-10	Sequence 10, Appl
21	92.5	3.6	325	2	US-08-842-045-10	Sequence 10, Appl
22	92.5	3.6	325	2	US-08-842-238-10	Sequence 10, Appl
23	92.5	3.6	325	3	US-08-629-335B-10	Sequence 10, Appl
24	92	3.6	944	4	US-09-134-001C-4352	Sequence 4352, Ap
25	90.5	3.6	378	3	US-09-299-843A-66	Sequence 66, Appl
26	90.5	3.6	378	4	US-09-088-337B-66	Sequence 2, Appl
27	89.5	3.5	382	4	US-09-262-477-2	Sequence 3227, Ap
28	89.5	3.5	443	4	US-09-134-001C-3227	Sequence 4, Appl
29	88.5	3.5	383	1	US-08-196-989B-4	Sequence 4, Appl
30	88.5	3.5	383	2	US-08-760-936-4	Sequence 5, Appl
31	88.5	3.5	480	1	US-09-041-075A-5	Sequence 2, Appl
32	88.5	3.5	1260	4	US-09-245-041-2	Sequence 2, Appl
33	88	3.5	370	1	US-08-415-818-12	Sequence 12, Appl
34	88	3.5	370	2	US-08-894-236-12	Sequence 12, Appl
35	88	3.5	370	5	PCT-US96-01444-12	Sequence 2, Appl
36	87.5	3.4	296	2	US-08-467-948A-2	Sequence 2, Appl
37	87.5	3.4	296	3	US-08-467-947A-2	Sequence 3507, Ap
38	87	3.4	445	4	US-09-134-001C-3507	Sequence 50, Appl
39	87	3.4	1843	4	US-09-413-814-50	Sequence 2, Appl
40	86.5	3.4	378	4	US-09-082-088-2	Sequence 2, Appl
41	86.5	3.4	378	4	US-09-546-117-2	Sequence 2, Appl
42	86.5	3.4	382	4	US-09-542-733-2	Sequence 4, Appl
43	86.5	3.4	3079	5	PCT-US94-00198-4	Sequence 6, Appl
44	86	3.4	317	1	US-08-118-270-6	Sequence 6, Appl
45	86	3.4	317	5	PCT-US93-08528-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-09-058-489-46
; Sequence 46, Application US/09058489
; Patent No. 6103886
; GENERAL INFORMATION:
; APPLICANT: Whitehead Institute for Biomedical Research
; APPLICANT: Lahn, Bruce
; APPLICANT: Page, David
; TITLE OF INVENTION: Genes in the No. 6103886-Recombining Region of
; TITLE OF INVENTION: the Y Chromosome
; FILE REFERENCE: WHI97-08PA
; CURRENT APPLICATION NUMBER: US/09/058,489
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/041,877
; EARLIER FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 46
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Human
US-09-058-489-46

Alignment Scores:
Pred. No.: 7.49e-11
Score: 169.00
Percent Similarity: 56.82%
Best Local Similarity: 34.85%
Query Match: 6.65%
DB: 3
Gaps: 2

US-09-768-781-2 (1-1389) x US-09-058-489-46 (1-129)

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Db 6 SerileAlaaspAspIlePheProLeuileSer-CysValGlyAlaIleHisCysAsnII 25

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Qy 702 GTTGGCTATCCAGATCAAGTACTAGTACGCTTGGCCCTAGAGTCT 761
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Db 25 eLeuAlaIleArgThrGlyAsnAapPheAlaAlaIleLysLeuValIleLysLeuI 45
:|||||:
Qy 762 CTGCATCACCATCTGGCGGAGCATTGGAGATCATCTCCGCCCTCCGTGCTCTT 821
: : : : :
Db 45 eTyrLeuMetIleTrpHisSerLeuValIleIleSerProValValThrLeuAlaPhePh 65
:|||||:
Qy 822 CTCAGCCACTTTGAATGAAGGTGCTGCCCTCTCTAGTGTCACTTCCGTGATCATCT 881
:|||||:
Db 65 eProAlaSerLeuLysGlnGlySerLeuHisPheLeuLeuIleIleTrpPheValLeuLe 85
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Qy 882 CTTTGAGCCCTGGATTAAGTCTGAGAGTGGTGGCCAGATGCCCAATAACATTGAGAA 941
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Qy 942 AAACCTCAGCCGGTGGCAGCTCTGGTGG-----TCCTGATTTTCAGTCACCAT 989
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Db 105 leIleProAla-----TrpTrpValSerMetAspAla-TyrLeuAsnHisAla 120
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Db 121 SerIleCysHisGln-PheSerCys 129
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RESULT 2
US-09-134-001C-5655
; Sequence 5655, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134.001C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5655
; LENGTH: 800
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5655
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Score: 114.00 Matches: 96
Percent Similarity: 40.14% Conservative: 81
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Query Match: 4.48% Indels: 129
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:|||||:
Qy 132 TACTTTTCCATTAGCATCTTTCTCCACCTTTTGTACTGTGGGAGGCTGCATCT-- 189
: : : : :
Db 422 pGlnTyrGlyPheValLeuThrPhe---ValIleSerIleGlyValIleAlaSerIl 441
:|||||:
Qy 190 -----GCTTTGTACATGTTAGTATCTATCGAAGAATAGTGAACATTA 233
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Db 441 eLeuThrPheThrTyrAlaLeuTyrMetIleLys-----GluThrPhe 455
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Qy 234 CTGATGACATACACCTTTTCTCTTTT-----ATGTT 266
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Qy 327 ACCGCTA-----TCATTATTATGATCTAATCTCTCTTGGGACCTGTTAT 371
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Qy 372 CAGATGT-----TTGGAGGCCATGATTAAAGTACCTCACACTGTG 410
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Db 505 rArgSerValSerGlyIleGlyAlaGluValAspAlaPheValProHisIleSerGlnTr 525
:|||||:
Qy 411 CAAGAAAGAGGAGGAGGAGGAGCCCTATGTC---AGCCTCACCCCGAAAGAAAGATGCTAT 467
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Db 525 p-----HisGlyValAsnLeuProLeuIleLeuSerIleVal-----ValIleIl 540
:|||||:
Qy 468 AGATGGC-----GAGGAGGTGCTGATAGATGG---GAGGTGGGCCACTTCCATCGGAC 518
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Db 540 eIleGlyLeuIleLeuAlaLeuValValAsnTrpLysGluValThrHisGlnIleIleLy 560
:|||||:
Qy 519 CCTGGCTATGCCCGCAATGCTACAAAGTATGTCACAG----- 558
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Db 560 sSerAlaSerIleThrAspGlyTyrArgLysIleTyrArgGluPheGluLeuTyrSerAl 580
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Qy 559 -----ATCCAAGCCTTCTCGGCTCAGTCCCGCAGCTGACCTATCAGCTCTATGTGAG 611
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Db 580 aArgGlyIleArgAlaLeuMetAsnAsn-----LysLeuAsnTyrTyrIleMetIleTh 598
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Qy 1126 -----ATGGTCTTGGTTTTTAAGTCTTCTTGGAGTGAAGTGTACTGATTA 1172
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Db 217 AspAlaHisSerPheAlaValIleLeu-----AlaMetGlyLeu 229
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Db 230 ValLeuTyrMetValThrIleIleLysGlnAspTyrAspValPheAsnLeuLeuLeu 249
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Db 250 -----LeuAsnIleGlyMetIleGluLeuTyrLeuSerAsnSerArgHisIlePhe 266
QY 679 TATGGGCCACCTTTGCAATATGTTGCTATCCAGATCAAGTAGTAGTACACAGATT 738
Db 267 IleSerValIleLeuCysLeuMetLeuLeuLeuProLeuSerHisIleLysLysArgIle 286
QY 739 CGC-----CTTGGGCCACTAGAGTCTCTGCATCACCATCTGGCGGACATGGAG 789
Db 287 LysHisProIleIleGlyAlaMetIleLeuMetAlaIleAlaIle-----TTC 822
QY 790 ATCACTTCCCGCCTCTGATCTGTGTGTC----- 822
Db 307 IleTyrHisLeuPheIleLysLeuLeuLysGlyLysAsnSerGlnGluValPheMet 326
QY 823 TCAGCCACTTTGAATGAAGCTGTG-----CCCTTCTCTAGTG 861
Db 327 ProSerAspMetAsnIleLysAlaIleAspTyrAlaLeuThrGluHisProPheLeuGly 346
QY 862 CTCAACTTCTGTATCATCTCTTTGAGCGCTGGATTAGTTCTGGAGAGTGGTCCCCAG 921
Db 347 SerGlyPheGlyIle-----ProMetIleLys----- 355
QY 922 ATGCCCAATAACATTGAGAAAAAATTACAGCGGTCGCGACTCTGGTGGTCTGTGATTCA 981
Db 356 -----AlaSerSerGluIleGlnTyrPheAsnValAlaThrSerAsnIleIlePheGly 373
QY 982 GTACCAATCTCTATGTGGCATCAACTTCTCTGCTGCTCAGCTTTGCGAGTTGAGGTTG 1041
Db 374 Met---IleIlePheThrGlyIle----- 380
QY 1042 GCAGACAGATCTCGTCGACAAAGGCGAGAACTGGGACATATGGGCTGCATATAGT 1101
Db 381 -----IleGlyLeuThrLeuCys 386
QY 1102 GTGAGTTGGTAGAGATGTCATCATGTCTTGGTTTAAAGTTCTTTGGAGTGAAGTG 1161
Db 387 ThrIleTyrMetLeuHisMetValLeuLeuValThrPhePro---MetSerIleThrIle 405
QY 1162 TTACTGAATTAATCTCATCTTGTATTCCTTGGAGCTCATTTATGCTTAT---CTGATT 1218
Db 406 LeuLeuPheLeuIleThrIlePheValAsnMetAspTyrIleIleLeuPheAspSerVal 425
QY 1219 TCCATTGGCTTCATGCTCTCTTTCTTCAGTACTTTCATTCATTCGCTCCTCTCTACC 1278
Db 426 GlyLeuGlyIleLeuCysTyrIlePheTrpGlyIleTyrLeuLysGluGlyMetTyrGln 445
QY 1279 CATAT 1284
Db 446 TyrAsn 447

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RESULT 5

US-08-612-986-5

; Sequence 5', Application US/08612986

; Patent No. 5770384

```

; GENERAL INFORMATION:
; APPLICANT: Elliot J. Androphy
; APPLICANT: Dave E. Breiding
; TITLE OF INVENTION: E2 BINDING PROTEINS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive & Cockfield
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/612,986
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/361,806
; FILING DATE: 22 DEC 1994
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Paul L.
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: NEP-004DV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-612-986-5

Alignment Scores:
Pred. No.: 0.0288 Length: 357
Score: 96.50 Matches: 35
Percent Similarity: 37.61% Conservative: 9
Best Local Similarity: 29.91% Mismatches: 56
Query Match: 3.79% Indels: 17
DB: 1 Gaps: 4

US-09-768-781-2 (1-1389) x US-08-612-986-5 (1-357)
QY 273 CATTATGTCAGTTGACCTCATTTTGTCCACAGAGATCTAGCCAAAGATAAACCGCT 332
Db 220 HisTyrGlyProThrGlnProAlaTyrSerProSerGlnGlnLeuArgAlaProSerAla 239
QY 333 ATC-----ATTATTTATGCATCTAATCTCTTGGGACCTGTATCATCATGTTTGGAGCC 386
Db 240 PheProAlaValGlnTyrLeuSerGlnProGlnHisGlnProTyrAlaValHisGlyHis 259
QY 387 CATGATTAAGTACCTCACACTGTGGAGAAAGAGAGGAGGAGGAGCCCTATGTGAGCCT 446
Db 260 PheGln-----ProThrGlnThrGlyPheLeuGlnProGlyGlyAlaLeuSerLeuGln 277
QY 447 CACCCGAAAGAGATGCTAATAGATGCGAGAGAGTGTGTAGTAAGTGGAGGTGGGCCA 506
Db 278 LysGlnMetGluHisAlaAsnGlnThrGlyPheSerAspSerSerSerLeuArgPro 297
QY 507 -----CTCCATCCGAGCCCTGGCTATGACCCCAATGCTGTACAAAGCTAT 551
Db 298 MethHisProGlnAlaLeuHisProAlaProGly-----Leu 309
QY 552 GTCACAGATCCAAGCCTTCTGGGCTCAGTGCCTCCAGCTGACCTATCAGCT 602
Db 310 LeuAlaSerProGlnLeuProValGlnMetGlnProAlaGlyLysSerAla 326

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RESULT 6

US-08-361-806A-5
; Sequence 5, Application US/08361806A
; Patent No. 5792833
; GENERAL INFORMATION:
; APPLICANT: Elliot J. Androphy
; APPLICANT: Dave E. Breiding
; TITLE OF INVENTION: E2 BINDING PROTEINS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive & Cockfield
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/361,806A
; FILING DATE: 22 DEC 1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Paul L.
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: NEP-004
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-361-806A-5

Alignment Scores:
Pred. No.: 0.0288 Length: 357
Score: 96.50 Matches: 35
Percent Similarity: 37.61% Conservative: 9
Best Local Similarity: 29.91% Mismatches: 56
Query Match: 3.79% Indels: 17
DB: 1 Gaps: 4

US-09-768-781-2 (1-1389) x US-08-361-806A-5 (1-357)

QY 273 CATTATGTCAGTTGACCTCATTTTGTCCAGAGATCTAGCCAAAGATAAACCGCT 332
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Db 220 HistyrglyProThrGlnProAlaty-SerProSerGlnLeuAlaProSerAla 239
QY 333 ATC-----ATTATTTATGATCTAATCTCTGGGACCTGTTATCAGATGTTTGGAGGC 386
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Db 240 PheProAlaValGlnTyrLeuSerGlnProGlnHisGlnProTyrAlaValHisGlyHis 259
QY 387 CATGATTAAGTACCTCACACTGTGGAAGAGAGAGGAGGAGGAGCCCTATGTCAGCCT 446
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Db 260 PheGln-----ProThrGlnThrGlyPheLeuGlnProGlyGlyAlaLeuSerLeuGln 277
QY 447 CACCCGAAGAAGATGCTAATAGATGGGAGGAGTGTCTAGATAGATGGGAGTGGGCCA 506
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Db 278 LysGlnMetGluHisAlaAenGlnGlnThrGlyPheSerAspSerSerLeuArgPro 297
QY 507 -----CTCCATCCGGACCTGGCTATGACCGCAATGCTTACAAACGCTAT 551
|||
Db 298 MethHisProGlnAlaLeuHisProAlaProGly-----Leu 309
QY 552 GTCCACAGATCCAGCTTCTGGGCTCAGTGCCTCCAGCTGACCTATCAGCT 602
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Db 310 LeuAlaSerProGlnLeuProValGlnMetGlnProAlaGlyLysSerAla 326

RESULT 7

PCT-US95-16806A-5
; Sequence 5, Application PC/TUS9516806A
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: E2 Binding Proteins
; NUMBER OF SEQUENCES: 21
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/16806A
; FILING DATE: December 22, 1995
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: US 08/361,806
; FILING DATE: 22-DEC-1994
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-16806A-5

Alignment Scores:
Pred. No.: 0.0288 Length: 357
Score: 96.50 Matches: 35
Percent Similarity: 37.61% Conservative: 9
Best Local Similarity: 29.91% Mismatches: 56
Query Match: 3.79% Indels: 17
DB: 5 Gaps: 4

US-09-768-781-2 (1-1389) x PCT-US95-16806A-5 (1-357)

QY 273 CATTATGTCAGTTGACCTCATTTTGTCCAGAGATCTAGCCAAAGATAAACCGCT 332
|||||
Db 220 HistyrglyProThrGlnProAlaty-SerProSerGlnLeuAlaProSerAla 239
QY 333 ATC-----ATTATTTATGATCTAATCTCTGGGACCTGTTATCAGATGTTTGGAGGC 386
|||
Db 240 PheProAlaValGlnTyrLeuSerGlnProGlnHisGlnProTyrAlaValHisGlyHis 259
QY 387 CATGATTAAGTACCTCACACTGTGGAAGAGAGAGGAGGAGGAGCCCTATGTCAGCCT 446
|||
Db 260 PheGln-----ProThrGlnThrGlyPheLeuGlnProGlyGlyAlaLeuSerLeuGln 277
QY 447 CACCCGAAGAAGATGCTAATAGATGGGAGGAGTGTCTAGATAGATGGGAGTGGGCCA 506
|||
Db 278 LysGlnMetGluHisAlaAenGlnGlnThrGlyPheSerAspSerSerLeuArgPro 297
QY 507 -----CTCCATCCGGACCTGGCTATGACCGCAATGCTTACAAACGCTAT 551
|||
Db 298 MethHisProGlnAlaLeuHisProAlaProGly-----Leu 309
QY 552 GTCCACAGATCCAGCTTCTGGGCTCAGTGCCTCCAGCTGACCTATCAGCT 602
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RESULT 8

US-09-134-001C-5576
; Sequence 5576, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C

; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5576
; LENGTH: 683
; TYPE: PRN
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5576

Alignment Scores:
Pred. No.: 0.0415 Length: 683
Score: 96.50 Matches: 82
Percent Similarity: 38.50% Conservative: 77
Best Local Similarity: 19.85% Mismatches: 151
Query Match: 3.79% Indels: 103
DB: 4 Gaps: 19

US-09-768-781-2 (1-1389) x US-09-134-001C-5576 (1-683)

Qy 262 ATGTTTTCATCATATGTCAGTCAGTCAGTCATTT-----TTTGTCCACAGA 309
Db 7 IlePheGluThrLeuLeuPheValAlaLeuValIleValSerSerPheValHisThr 26
Qy 310 GATCAGCCAAAGATAAACCCCTATCATATTTATGTCATCTAATCCTCTTGGACCTGTT 369
Db 27 PheIleProLys-----ValProLeuAlaPheIleGln-----IlePheLeuGly----- 41
Qy 370 ATCAGATGTTTGGAGGCCATGATTAAAGTACCTCACACTGTGGAGAAAGAG----- 420
Db 42 -----MetIleLeuTyrluThrProIleProValGluPheAsnPhe 55
Qy 421 GAGCAGAGGAGCCCTATGTCAGCCTCACCGAAGAGATGCTAATAGATGGCGAGGAG 480
Db 56 AspSerGluLeuPheMetValThrLeuIleAlaProLeuLeuPheValGluGly----- 73
Qy 481 GTGCTGATAGATGGAGGTGGGCCACTCCATCCGACCTGGCTATGACCGCAATGCC 540
Db 74 -----ValAsnValSerArgValHisLeuArgLys 83
Qy 541 TACAAAGCTATGTACAGATCCAAAGCTTCTCTGGGCTCAGTG-----CCCCAGCTGACC 594
Db 84 TyrlleLysProValMetMetMetAla---LeuGlyLeuValIleThrValIleGly 102
Qy 595 TATCAGCTCTATGAGGCTGATCTCTGACAGAGTTCCTGGGTAGAGTGTGTCTAATG 654
Db 103 ValGlyLeuPheIleHisTrpIleTrpProGluLeuProIleGlyAlaAlaPheAlaIle 122
Qy 655 GTATTTTCCCTG----- 666
Db 123 AlaAlaIleLeuCysProThrAspAlaValAlaValGlnAlaIleThrLysGlyLysVal 142
Qy 667 -----GTATCTGTACCTATGCGGCCACCTTTGCAATATGTTGGCTATC 711
Db 143 LeuProLysGlySerMetThrIleLeuGluGlyGluSerLeuLeuAsnAspAlaIleGly 162
Qy 712 CAGATCAAGTACGATGACTACAGATTCGCTTGGGCCACTAGAGTCTCTGCATCACC 771
Db 163 IleIle-----SerPheLysIleAlaValGlyValLeuIleThrGlyThrPheSer 179
Qy 772 ATCTGGGGGACATTTGGAG-----ATCACTTCC-----CGCTTC 804
Db 180 IlePheAspAlaIleGlnGlnPheLeuIleAlaSerIleGlyAlaIleValGlyLeu 199
Qy 805 CTGATT-----CTGCTGCTTCTCAGCCACTTTTGAATTTGAAGCTGTGCCCTTC 855
Db 200 IleIleGlyMetAlaLeuValArgPheArgLeuThrMetArgArgGlyIleIleuAsn 219
Qy 856 CTAGTGTCTCACTTCTCTGATCATCTCTTCTGAGCCCTGGATTAAGTCTTGGAGAGTGGT 915
Db 220 IleAsnMetPheThrPheIleGlnLeuLeuThrProPheValThrTyrlu----- 236

Qy 916 GCCCAGATGCCCAATAACATTGAGAAAACCTTCAGCCGGTGGCAGCTCTGTGGTCTCTG 975
Db 237 -----IleAlaGluLeuPheHisAlaSerGlyIleIleAlaAlaVal 250
Qy 976 ATTTCAATCACCATCCTCTATGCTGGCATCAACTTCTCTGCTGCTGCTGCTGCTG 1035
Db 251 Val-----AlaGlyLeu-----Val 255
Qy 1036 AGTTGGCAGACAGAGATCTCGTGACAAAGGGCAGAACTATGGGACATATGGCCCTGCAC 1095
Db 256 HisGlyPheGluArgAspArgIleAlaGlnThrArgThrGlnLeuGlnMetSerTyrluAsn 275
Qy 1096 TATAGTGTGAGTGTGGTAGAGAATGTGATCATGTGCTTGGTGTGTTTAAAGTCTTTCGA 1152
Db 276 HisThrTrpSerIleLeuGlyTyrluValLeuAsnGlyPheValPheSerIleLeuGlyPhe 295
Qy 1153 -----GTCAAAGTGTACTGTAATTAATGCTCATCTCTGATTCCTGATTCGCTTG 1194
Db 296 LeuValProGluValIleValIleValIleValIleValIleValIleValIleValIle 315
Qy 1195 CAGCTCATATTGCTTATCTGATTTCCATTTGGCTTTCATGCTCTCTTTCTTCCAGTACTTG 1254
Db 316 ---IleValIleThrLeuLeuValAlaLeuAlaValTyrluPheArgPheValIrluVal 334
Qy 1255 CATCATTTGCGCTCCTCTTCCACCATTAATGTAGTAGACTACTCCATTTGCTGCTGCTGT 1314
Db 335 TyrluLeuTyrluProTyrluPheTyrluSerValSerProPheGlnLysMetIle----- 352
Qy 1315 CACCAGCACCTCGACCGAGGTTGAGAACTCAGAGCCA 1353
Db 353 SerLysAsnAspGluAspLysValThrGluSerLysPro 365

RESULT 9

US-08-415-818-6
; Sequence 6, Application US/08415818
; Patent No. 5621079
; GENERAL INFORMATION:
; APPLICANT: Cascieri, Margaret A.
; APPLICANT: Linemeyer, David L.
; APPLICANT: MacNeil, Douglas J.
; APPLICANT: Shiao, Lin-Lin
; APPLICANT: Strader, Catherine D.
; APPLICANT: Tan, Carina P.
; APPLICANT: Weinberg, David H.
; TITLE OF INVENTION: NEUROPEPTIDE Y RECEPTOR
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mary A. Appollina
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/415,818
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/383,746
; FILING DATE: 03-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Appollina, Mary A.
; REGISTRATION NUMBER: 34,087
; REFERENCE/DOCKET NUMBER: 19390
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-594-3462
; TELEFAX: 908-594-4720

: INFORMATION FOR SEO ID NO: 6:

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; INFORMATION FOR SEQ ID NO:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 371 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-415-818-6

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Alignment Scores:

Pred. No.:	0.0336	Length:	371
Score:	96.00	Matches:	78
Percent Similarity:	37.39%	Conservative:	85
Best Local Similarity:	17.89%	Mismatches:	153
Query Match:	3.78%	Indels:	120
DB:	1	Gaps:	18

US-09-768-781-2 (1-1389) x US-08-415-818-6 (1-371)

QY	116	GAGCCACCCCGAT-----TTACTTTTCCATTATGCA	148
DB	7	GlnProThrProLeuLysThrSerGlyLysSerAsnAsnSerAlaPhePheTyGlyPheGlu	26
QY	149	TCCTTTTCTCCACCTTTTGTGTACTGTGGGAGGCTGCATCTGCTTTGTGTACATGTTAGAA	208
DB	27	SerCysGlnProProPheLeuAlaLeu-----LeuLeuLeuLeuLeuAlaTy	42
QY	209	TCTATCGAAAGAATAGTGAACACTTACTGGATGACATACACCTTTCTTTCTTTATGTTTT	268
DB	43	ThrValIleLeuIleMetGlyIlePheGly-AsnLeuSerLeuIleIleIleIle-----	60
QY	269	CATCCATTATGGTCCAGCTTGCACCTCATTTTGTCTCCACAGAGATCTAGCCAAAGATAAAC	328
DB	61	-----PheLysLysGlnArgGluAlaGlnAsnValTh	71
QY	329	CGCTATCATTTATT-----TATGCATCTAATCTCTTGGGACCTGTTATCAGATGTTTCG	382
DB	71	raenIleLeuIleAlaAsnLeuSerAspIleLeuValCys-ValMetCysIleP	91
QY	383	AGGCCATGATTAAGTACTCTCACACTGTGGAAGAAAGAGGACGAGGAGCCCTATGTCA	442
DB	91	roPheThrValIleTy-----ThLeuMetAsp-----HisTrpValPheG	105
QY	443	GCCTCACCCGAAAGATGCTAATATAGATCGCGAGGAGGTGCTCATAGTAATGGAGGTGG	502
DB	97	-----ThLeuMetAsp-----HisTrpValPheG	105
QY	503	GCCACTCCATCCGAGCCCTGGCTATGACCGCGCAATGCTACAAACGATGTGTACACATCC	562
DB	105	lyAanThrMetCysLysLeu-----ThrSerTyValGlnSerValSerValS	121
QY	563	AGCCTTCCTGGGCTAGTGGCCCGACCTGACCTATCAGCTCTATGTGAGCGTGATCTCTG	622
DB	121	erValSerIlePheSerLeuValLeuIleAlaIleGluArgTyGlnLeuIleValAsnP	141
QY	623	CAGAGGTTCCTCCCTGGGTAGAGTTGTG-----CTAATGGTATTTCCTCCCTGG	667
DB	141	roArgGlyTyTrpLysProArgValAlaHisAlaTyTrpGlyIleIleLeuIleTrpLeu	161
QY	668	TATCTGTCACTATGGGGCCACCTTTGGCAATATGTTGGCTATCCAGATCAAGATCAGATG	727
DB	161	leSerLeuThrLeuSerIleProLeu-----PheLeuSerTyHisLeuThrAsnGluP	179
QY	728	ACTACAAGATTCCGCTTGGGGCCACTA-----GAAGTCCTCTGCATCACCACCA	772
DB	179	roPheHisAsnLeuSerLeuProThrAspIleTyThrHisGlnValAlaCysValGluI	199
QY	773	TCTGGCGGACATTTGGAGATCACTTCCCGCCTCTCGATTCTGGTGCCTCTCTCAGCCACTT	832
DB	199	leIrrProSer-----LysLeuAsnGlnLeuLeuPheSerThrSerL	213
QY	833	TGAATTGAAGGTGTGCCCTTCTAGTGTCTCAACTTCCTGTATCATCTCTTTGAGCCCT	892
DB	213	euPheMetLeuGlnTy-----PheValProLeuGlyPheIleLeuIleCysTyTrpLeuVal	232

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 371 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; LIBRARY: GenBank

; CLONE: 1378004

; US-08-919-624-4

Alignment Scores:

Pred. No.: 0.0336 Length: 371
 Score: 96.00 Matches: 78
 Percent Similarity: 37.39% Conservative: 85
 Best Local Similarity: 17.89% Mismatches: 153
 Query Match: 3.78% Indels: 120
 DB: 2 Gaps: 18

US-09-768-781-2 (1-1389) x US-08-919-624-4 (1-371)

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QY 116 GAGCCACCCCGAT-----TTACTTTTCCATTAGCA 148
Db 7 GlnProThrProAsnLysThrSerGlyLysSerAsnSerAlaPhePheTyrPheGlu 26
QY 149 TCCTTTTCTCCACCTTTTGTACTGTGGGAGGCTGCATCTGCTTTGTACATGGTTAGAA 208
Db 27 SerCysGlnProPheLeuAlaile-----LeuLeuLeuLeuLeuLeuAlaTyr 42
QY 209 TCTATCGAAGAAGATAGTGAACCTTACTGTGATGACATACACCTTTTCTTTTATGTTTT 268
Db 43 ThrValIleLeuIleMetGlyIlePheGly-AsnLeuSerLeuIleIleIleIle----- 60
QY 269 CATCCATTATGGTCCAGTTCACCTTCATTTTGTCCACAGAGATCTAGCCAAAGATAAAC 328
Db 61 -----PheLysLysGlnArgGluAlaGlnAsnValTh 71
QY 329 CGCTATCATATT-----TATGCATCTAATCTCTTGGGACCTGTTATCAGATGTTGG 382
Db 71 rAnIleLeuIleAlaAsnLeuSerLeuSerAspIleLeuValCys-ValMetCysIleP 91
QY 383 AGCCATGATTAAATGATCACTCAGCTGTGGAAGAAAGAGGAGGAGGAGCCCTATGTCA 442
Db 91 roPheThrValIleTyr-----HisTrpValPheG 502
QY 443 GCCTACCCGAAAGAGATGTAATAGATGCGGAGGAGTCTGATGATGAGATGGAGGTGG 502
Db 97 -----ThrLeuMetAsp-----HisTrpValPheG 105
QY 503 GCCACTCCATCCGACCTCGCTATGATGACCCCAATGCTACAAAGCTATGTCAGATCC 562
Db 105 lYAsnThrMetCysLysLeu-----ThrSerTyrValGlnSerValSerValS 121
QY 563 AAGCTTCTCTGGGCTAGTGGCCCGACCTATGATGAGCTATGAGCTGAGCTGATCTCTG 622
Db 121 erValSerIlePheSerLeuValLeuIleAlaIleGluArgTyrGlnLeuIleValAsn 141
QY 623 CAGAGGTTCCTCGGTAGAGTTGTG-----CTAATGGTATTTTCCCTGG 667
Db 141 roArgGlyTyrPysProArgValAlaHisAlaTyrTrpGlyIleIleLeuIleTrpLeu 161
QY 668 TATCTGTCACTATGGGGCCACCCTTTGCAATATGTTGGCTATCCAGATCAAGTACAGT 727
Db 161 leSerLeuThrLeuSerIleProLeu-----PheLeuSerTyrHisLeuThrAsnGlu 179
QY 728 ACTACAAGATTGCGCTTGGGCACTA-----GAAGTCTCTGCATCACA 772
Db 179 roPheHisAsnLeuSerLeuProThrAspIleTyrThrHisGlnValAlaCysValGlu 199
QY 773 TCTGGGAGCATTTGGAGATCACTTCCCGCTCTCTGATTTCTGCTCTCTTCAGCCACTT 832
Db 199 leTrpProSer-----LysLeuAsnGlnLeuLeuPheSerThrSerL 213

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QY 833 TGAATTTGAAGGCTGTGCCCTTCTAGTGTCTCAACTTCTCTGATCATCTCTTTTGAGCCCT 892
Db 213 euPheMetLeuGlnTyr---PheValProLeuGlyPheIleLeuIleCysTyrLeuLysI 232
QY 893 GGATTAACTTCTGGAGAAGTGTGCCAGATGCCCAATAACATTAGAGAAAATCTTCAGCC 952
Db 232 leValLeuCysLeuArgLysArgThrArgGlnValAspArgArgLysGluAsnLysSerA 252
QY 953 GGGTCGGC-----ACTCGTGGTCTCTGATTTTCACTCACCATCTCTCTATGCTG 1000
Db 252 rGLeuAsnGluAsnLysArgValAsnValMetLeuIleSerIleValValThrPheGly- 271
QY 1001 GCATCAACTTCTCTGCTGTCAGCTTTGTCAGTTGAGGTTGGCAGACAGAGATCTCGTCG 1060
Db 272 -----AlaCysTrpLeuProLeuAsn----- 278
QY 1061 ACAAAGGCGAAGCTGGGACATATGGGCGCTGCACATATAGTGTGAGGTTGGTAGAATG 1120
Db 278 ----- 278
QY 1121 TGATCATGGTCTTGGTTTAAAGTTCTTTGGAGTGAAAGTGTACTGAATTACTGTCAAT 1180
Db 279 --IlePheAsnValIlePheAspTrpTyrHis---GluMetLeuMetSerCysHisHis 297
QY 1181 CTTGATTGCTTGCAGCTCATTATTGCTTATCTGATTTCCATTGGCTTCATGCTCTTT 1240
Db 297 spLeuValPheValValCysHisLeuIleAlaMetValSerThrCysIleAsnProLeuP 317
QY 1241 TCTTCCACTACTTGCATCCATTGGCTCCTCTTCCACCCATAATAGTAGAGACTACCTCC 1300
Db 317 heTyrGlyPheLeuAsn-----LysAsnPheGlnLysAspLeuMetMetLeuIleH 334
QY 1301 ATTGTGCTGCTGCACGACGACCTCGGACACGAGGTTGAGAAC 1344
Db 334 iHisCysTrpCysGlyGlu---ProGlnGluSerTyrGluAsn 347

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RESULT 12

PCT-US96-01444-6

; Sequence 6, Application PC/TUS9601444

; GENERAL INFORMATION:

; APPLICANT: Cascieri, Margaret A.

; APPLICANT: Linemeyer, David L.

; APPLICANT: MacNeil, Douglas J.

; APPLICANT: Shiao, Lin-Lin

; APPLICANT: Strader, Catherine D.

; APPLICANT: Tan, Carina P.

; APPLICANT: Weinberg, David H.

; TITLE OF INVENTION: NEUROPEPTIDE Y RECEPTOR

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Mary A. Appollina

; STREET: P.O. Box 2000, 126 E. Lincoln Ave.

; CITY: Rahway

; STATE: NJ

; COUNTRY: USA

; ZIP: 07065

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US96/01444

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/383,746

; FILING DATE: 03-FEB-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/415,818

; FILING DATE: 03-APR-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Appollina, Mary A.

Qy	22	TCAGAAAGAACTCGACATGGACAGAGTTTATGAAATT	-----CTGAGGAG 69
Db	83	SerGluArgThrSer-----LysHisValTyLysLeuLeuLysGlyCysProThrPro	100
Qy	70	CCAAATGTGGATCCGGTTTCA	-----TCCTGGAG 99
Db	101	ProTrpAlaAlaProGlySerGlyThrGlyCysCysAlaGlyArgTrpGlnAlaLeuGlu	120
Qy	100	GAAGATGTCATCCGTGAGCAACCCC	-----126
Db	121	Ser-----GlyAlaSerProAlaArgLeuSerSerLeuThrSerAlaTrpSer	136
Qy	127	-----CGATTACTTTTCATTTTAGCATCTTTCTCCACCTTTTGTACTGTGG	177
Db	137	GlnGlyLeuArgGlyThrAlaPro-LeuGlnAlaGlyArgSerProSerArgLeuLeuPr	156
Qy	178	GAGCTGCATCTGCTTTGTACATGGTTAGAAATCTATCGAAAGAATAAGTGAACCTTACTCG	237
Db	156	oArg--ProAlaLeuCysProTrpSerCysLeuArgArgAsnProThrSerProArgG	175
Qy	238	ATGACATACACCTTTCTTCTTTATGT--TTTCATCCATTATGTCAGCTGTGACCCCTC	294
Db	175	ySerSerThrProTrpAlaThrAlaSerArgLeuGlnProSerTrpProSer-----	192
Qy	295	ATTTTGTCCACAGAGATCTAGCCAAAGATAAACCGCTATCATTTATGCATCTAATC	354
Db	193	-----Se 193	
Qy	355	CTCTGGGACCTGTTATCAGATGTTTGGAGGCCA--TGATTAAGTACCTCACACTGTGG	411
Db	193	rSerTrpSerLeuSerGlySerThrAlaProGlyThrThrSerThrProSerCysSe	213
Qy	412	AAGAAAG--AGAGACAGGAGGAGCCCTATGTCAGCTCACCCGGAAGAAGATGCTAATA	468
Db	213	rProProLeuSerSerArgArgGlnLeuCysSerArgThrProProSerPhe-----	230
Qy	469	GATGGCGAGGAGTGCTGTAGTAATGGAGG--TGGGCCACTCCCATCCGACCTGGCT	525
Db	231	-----ThrGlyArgThrTrpThrAlaAlaSerProLeuSe	243
Qy	526	ATGCACCGCAATGCCTACAACGTAATGTCACAGATCCAAAGCCTTCTGGGCTCAGTGCC	585
Db	243	rCysAlaArgLeuLeuProProLeuLeuSerArg--ProProThrSerAlaGlyCys--	261
Qy	586	CAGCTGACCTATACAGTCTATGTGAGCCTGATCTCTGCAGAGGTTCCCTGGGTAGAGTT	645
Db	262	-----TrpGlnLysLe	265
Qy	646	GTGCTAATGGTATTTTCCCTGGTATCTGTCACTATGGGCGCCACCTTTGCCAATATGTTG	705
Db	265	uCys-----ThrProAlaSerProPro-----	272


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QY 1165 CTGAATTACTGTCATTCTTCCTTCGATTCGCTTCGAGCTCATTATTGCTTATCTGATTTCCATT 1224
|||::: :::::|||||::: |||||::: :::::
Db 219 LeuSerIleLeuLeuGlyIleValAlaLeuGluSerAlaIleAlaPheIleGlnAlaMet 238

QY 1225 GGCTTCATGCTCCTTTTCTTCCTCCAGTACTTG 1254
||| ::::| |||:::
Db 239 ValPheThrMetLeuThrCysSerTyrIle 248
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Search completed: April 1, 2003, 09:00:02
Job time : 34.5 secs